

-1-

SEQUENCE LISTING

<110> Vaccinex, Inc.
Robert, Bruno
Donda, Alena
Cesson, Valerie
Mach, Jean-Pierre
Zauderer, Maurice

<120> Targeted CD1d Molecules

<130> 1843.020PC00

<150> EP 02405838.0

<151> 2002-09-27

<160> 54

<170> PatentIn version 3.2

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial linker peptide

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial linker peptide

<400> 2

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser
1 5 10 15

<210> 3

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> F(ab)-avidin sense fragment

<400> 3

aattgcggcc gcaaaccatg ggatggagct gtatcatc

38

<210> 4

<211> 45

-2-

<212> DNA
<213> Artificial Sequence

<220>
<223> F(ab)-avidin antisense fragment

<400> 4
cggggtacct gaccaccgc ctcctttctt gtccacctg gtgtt 45

<210> 5
<211> 38
<212> DNA
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<220>
<223> F(ab')₂-avidin sense fragment

<400> 5
aattgcggcc gcaaaccatg ggatggagct gtatcatc 38

<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> F(ab')₂-avidin antisense fragment

<400> 6
cggggtacct gaccaccgc ctcctgggca cggtagggcat gtgtg 45

<210> 7
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1-avidin sense fragment

<400> 7
aattgcggcc gcaaaccatg ggatggagct gtatcatc 38

<210> 8
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1-avidin antisense fragment

<400> 8
cggggtacct gaccaccgc ctcctttacc cggagacagg gagag 45

<210> 9
<211> 40
<212> DNA
<213> Artificial Sequence

-3-

<220>

<223> Chick avidin sense primer

<400> 9

cggggtaccg gaggcgtgg gtcagccaga aagtgtcgc

40

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Chick avidin antisense primer

<400> 10

cgaccgtct cttctgtgt gcgcaggc

28

<210> 11

<211> 823

<212> DNA

<213> Artificial Sequence

<220>

<223> F(ab)-Avidin nucleotide construct

<400> 11

gcgccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60

cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcgggtct tccccctggc 120

accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta 180

cttccccgaa ccgggtgacgg tgctcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240

cttccccggct gtcctacagt cctcaggact ctactccctc agcagcgtcg tgaccgtgcc 300

ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360

caaggtggac aagaaaggag gcggtgggtc aggtaccgga ggcggtgggt cagccagaaa 420

gtgctcgtcg actgggaaat ggaccaacga tctgggctcc aacatgacca tcggggctgt 480

gaacagcaga ggtgaattca caggcaccta catcacagcc gtaacagcca catcaaatga 540

gatcaaagag tcaccactgc atgggacaca aaacaccatc aacaagagga cccagcccac 600

ctttggcttc accgtcaatt ggaagtttcc agagtccacc actgtcttca cgggccagtg 660

cttcatagac aggaatggga aggaggtcct gaagaccatg tggtcgtgc ggtcaagtgt 720

taatgacatt ggtgatgact ggaaagctac cagggtcggc atcaacatct tctctgcct 780

gcgcacacag aaggagaccg gtcacatca ccatcaccat tga 823

<210> 12

<211> 269

<212> PRT

<213> Artificial Sequence

-4-

<220>

<223> F(ab)-Avidin polypeptide construct

<400> 12

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Gly Gly Gly Gly Ser Gly Thr
 115 120 125

Gly Gly Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr
 130 135 140

Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly
 145 150 155 160

Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu
 165 170 175

Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg
 180 185 190

Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser
 195 200 205

Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu
 210 215 220

Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly

-5-

225 230 235 240

Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu
245 250 255

Arg Thr Gln Lys Glu Thr Gly His His His His His His
260 265

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<210> 13
<211> 871
<212> DNA
<213> Artificial Sequence
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<220>
<223> F(ab')₂-Avidin nucleotide construct

<400>	13						
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cgcgcataatg	gtcaccgtct	cctcagcctc	caccaagggc	ccatcggtct	tccccctggc		120
accctcctcc	aagagcacct	ctggggggcac	agcggccctg	ggctgcctgg	tcaaggacta		180
cttccccgaa	cgggtgacgg	tgctgtggaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac		240
cttcccggct	gtcctacagt	cctcaggact	ctaactccctc	agcagcgtcg	tgaccgtgcc		300
ctccagcagc	ttgggcaccc	agacctacat	ctgcaacgtg	aatcacaagc	ccagcaacac		360
caaggtggac	aagaaagttg	agcccaaatc	ttgtgacaaa	actcacacat	gccaccgtg		420
cccaggaggc	ggtgggtcag	gtaccggagg	cggtgggtca	gccagaaagt	gctcgctgac		480
tgggaaatgg	accaacgatc	tgggctccaa	catgaccatc	ggggctgtga	acagcagagg		540
tgaattcaca	ggcacctaca	tcacagccgt	aacagccaca	tcaaattgaga	tcaaagagtc		600
accactgcat	gggacacaaa	acaccatcaa	caagaggacc	cagcccacct	ttggcttcac		660
cgtcaatttg	aagttttcag	agtccaccac	tgtcttcacg	ggccagtgct	tcatagacag		720
gaatgggaag	gaggtcctga	agaccatgtg	gctgctgcgg	tcaagtgtta	atgacattgg		780
tgatgactgg	aaagctacca	gggtcggcat	caacatcttc	actcgctgc	gcacacagaa		840
ggagaccggt	catcatcacc	atcaccattg	a				871

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<210> 14
<211> 285
<212> PRT
<213> Artificial Sequence
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<220>
<223> F(ab')₂-Avidin polypeptide construct

<400> 14

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

-6-

1	5	10	15
Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val	20	25	30
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala	35	40	45
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser	50	55	60
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val	65	70	75
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro	85	90	95
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys	100	105	110
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp	115	120	125
Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Gly Thr	130	135	140
Gly Gly Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr	145	150	155
Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly	165	170	175
Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu	180	185	190
Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg	195	200	205
Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser	210	215	220
Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu	225	230	235
Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly	245	250	255

-7-

Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu
 260 265 270

Arg Thr Gln Lys Glu Thr Gly His His His His His His
 275 280 285

<210> 15
 <211> 1522
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG1 Avidin nucleotide construct

<400> 15
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 cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc 120
 accctcctcc aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta 180
 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240
 cttccccggt gtcctacagt cctcaggact ctactccctc agcagcgctc tgaccgtgcc 300
 ctccagcagc ttggggaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360
 caaggtggac aagaaagttg agcccaaadc ttgtgacaaa actcacacat gcccaccgtg 420
 cccagcacct gaactcctgg ggggaccgtc agtcttcctc tccccccaa aaccaagga 480
 caccctcatg atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga 540
 agaccctgag gtcaagttca actggtacgt ggacggcgctg gaggtgcata atgccaagac 600
 aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg gtcagcgctc tcaccgtcct 660
 gcaccaggac tggctgaatg gcaaggagta caagtgaag gtctccaaca aagccctccc 720
 agcccccatc gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta 780
 caccctgccc ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt 840
 caaaggcttc tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa 900
 caactacaag accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa 960
 gctcaccgtg gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca 1020
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 cggtgggtca ggtaccggag gcggtgggtc agccagaaag tgctcgctga ctgggaaatg 1140
 gaccaacgat ctgggctcca acatgaccat cggggctgtg aacagcagag gtgaattcac 1200
 aggcacctac atcacagccg taacagccac atcaaatgag atcaaagagt caccactgca 1260
 tgggacacaa aacaccatca acaagaggac ccagcccacc tttggcttca ccgtcaattg 1320
 gaagttttca gagtccacca ctgtcttcac gggccagtgc ttcataagaca ggaatgggaa 1380

-8-

ggaggtcctg aagaccatgt ggctgctgcg gtcaagtgtt aatgacattg gtgatgactg 1440
 gaaagctacc agggctcggca tcaacatctt cactcgcctg cgcacacaga aggagaccgg 1500
 tcatcatcac catcaccatt ga 1522

<210> 16
 <211> 502
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 Avidin polypeptide construct

<400> 16

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His

-9-

180	185	190
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg		
195	200	205
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys		
210	215	220
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu		
225	230	235
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr		
245	250	255
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu		
260	265	270
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp		
275	280	285
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val		
290	295	300
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp		
305	310	315
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His		
325	330	335
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro		
340	345	350
Gly Lys Gly Gly Gly Gly Ser Gly Thr Gly Gly Gly Gly Ser Ala Arg		
355	360	365
Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met		
370	375	380
Thr Ile Gly Ala Val Asn Ser Arg Gly Glu Phe Thr Gly Thr Tyr Ile		
385	390	395
Thr Ala Val Thr Ala Thr Ser Asn Glu Ile Lys Glu Ser Pro Leu His		
405	410	415
Gly Thr Gln Asn Thr Ile Asn Lys Arg Thr Gln Pro Thr Phe Gly Phe		
420	425	430

-10-

Thr Val Asn Trp Lys Phe Ser Glu Ser Thr Thr Val Phe Thr Gly Gln
 435 440 445

Cys Phe Ile Asp Arg Asn Gly Lys Glu Val Leu Lys Thr Met Trp Leu
 450 455 460

Leu Arg Ser Ser Val Asn Asp Ile Gly Asp Asp Trp Lys Ala Thr Arg
 465 470 475 480

Val Gly Ile Asn Ile Phe Thr Arg Leu Arg Thr Gln Lys Glu Thr Gly
 485 490 495

His His His His His His
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<210> 17
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BirA Sense Sequence

<400> 17
 ccggtggtgg cgggtctgaac gacatcttcg aggctcagaa aatcgaatgg cacgaat 57

<210> 18
 <211> 57
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BirA Antisense Sequence

<400> 18
 ccggattcgt gccattcgat tttctgagcc tcgaagatgt cgttcagacc gccacca 57

<210> 19
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> E1 sense sequence.

<400> 19
 cacggtaccg atatggggtg cctgctgttt ctgc 34

<210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

-11-

<223> E1 antisense

<400> 20

cagaccgggtc cagtagagga cgatgtcctg

30

<210> 21

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Construct of nucleotide sequence for extracellular domain of CD1d

<400> 21

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ggtagcgata tgggggtgcct gctgtttctg ctgctctggg cgctcctcca ggcttgggga      60
agcgctgaag tcccgcaaag gcttttcccc ctccgctgcc tccagatctc gtccttcgcc      120
aatagcagct ggacgcgcac cgacggcttg gcgtggctgg gggagctgca gacgcacagc      180
tggagcaacg actcggacac cgtccgctct ctgaagcctt ggtcccaggg cacgttcagc      240
gaccagcagt gggagacgct gcagcatata tttcggggtt atcgaagcag cttcaccagg      300
gacgtgaagg aattcgccaa aatgctacgc ttatcctatc ccttggagct ccagggtgtcc      360
gctggctgtg aggtgcaccc tgggaacgcc tcaaataact tcttccatgt agcatttcaa      420
ggaaaagata tcctgagttt ccaaggaact tcttgggagc caaccaaga ggccccactt      480
tgggtaaact tggccattca agtgctcaac caggacaagt ggacgaggga aacagtgcag      540
tggctcctta atggcacctg cccccaattt gtcagtggcc tccttgagtc aggggaagtcg      600
gaactgaaga agcaagtga gccaaggcc tggctgtccc gtggccccag tcctggccct      660
ggcgcgtctgc tgctggtgtg ccatgtctca ggattctacc caaagcctgt atgggtgaag      720
tggatgcggg gtgagcagga gcagcagggc actcagccag gggacatcct gcccaatgct      780
gacgagacat ggtatctccg agcaaccctg gatgtggtgg ctggggaggc agctggcctg      840
tcctgtcggg tgaagcacag cagtctagag ggccaggaca tcgtcctcta ctggaccggt      900
ggtggcggtc tgaacgacat cttcgaggct cagaaaatcg aatggcacga atccggtcat      960
catcaccatc accattga                                     ..      978

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<210> 22

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> Construct of polypeptide sequence for extracellular domain of CD1d

<400> 22

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp

-12-

1	5	10	15
Gly Ser Ala	Glu Val Pro Gln Arg	Leu Phe Pro Leu Arg	Cys Leu Gln
	20	25	30
Ile Ser Ser	Phe Ala Asn Ser Ser	Trp Thr Arg Thr	Asp Gly Leu Ala
	35	40	45
Trp Leu Gly	Glu Leu Gln Thr His	Ser Trp Ser	Asn Asp Ser Asp Thr
	50	55	60
Val Arg Ser	Leu Lys Pro Trp Ser	Gln Gly Thr Phe Ser	Asp Gln Gln
65	70	75	80
Trp Glu Thr	Leu Gln His Ile Phe	Arg Val Tyr Arg	Ser Ser Phe Thr
	85	90	95
Arg Asp Val	Lys Glu Phe Ala Lys	Met Leu Arg Leu Ser	Tyr Pro Leu
	100	105	110
Glu Leu Gln	Val Ser Ala Gly Cys	Glu Val His Pro	Gly Asn Ala Ser
	115	120	125
Asn Asn Phe	Phe His Val Ala Phe	Gln Gly Lys Asp	Ile Leu Ser Phe
	130	135	140
Gln Gly Thr	Ser Trp Glu Pro Thr	Gln Glu Ala Pro	Leu Trp Val Asn
145	150	155	160
Leu Ala Ile	Gln Val Leu Asn Gln	Asp Lys Trp Thr	Arg Glu Thr Val
	165	170	175
Gln Trp Leu	Leu Asn Gly Thr Cys	Pro Gln Phe Val	Ser Gly Leu Leu
	180	185	190
Glu Ser Gly	Lys Ser Glu Leu Lys	Lys Gln Val Lys	Pro Lys Ala Trp
	195	200	205
Leu Ser Arg	Gly Pro Ser Pro	Gly Pro Gly Arg	Leu Leu Leu Val Cys
	210	215	220
His Val Ser	Gly Phe Tyr Pro	Lys Pro Val Trp	Val Lys Trp Met Arg
225	230	235	240
Gly Glu Gln	Glu Gln Gln Gly	Thr Gln Pro Gly	Asp Ile Leu Pro Asn
	245	250	255

-13-

Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
 260 265 270

Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
 275 280 285

Gln Asp Ile Val Leu Tyr Trp Thr Gly Gly Gly Gly Leu Asn Asp Ile
 290 295 300

Phe Glu Ala Gln Lys Ile Glu Trp His Glu Ser Gly His His His His
 305 310 315 320

His His

<210> 23
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F(ab)-B2M sense construct

<400> 23
 aattgcgggcc gcaaaccatg ggatggagct gtatcatc

38

<210> 24
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F9ab)-B2M antisense construct

<400> 24
 cggggtacct gaccacccgc ctcctttctt gtccaccttg gtggtt

45

<210> 25
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F(ab')₂-B2M sense construct

<400> 25
 attgcggccg caaacatgg gatggagctg tatcatc

37

<210> 26
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

-14-

<223> F(ab')₂-B2M antisense construct

<400> 26

cggggtacct gaccaccgc ctcctgggca cggtgggcat gtgtg 45

<210> 27

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> IgG1-B2M sense construct

<400> 27

aattgcggcc gcaaaccatg ggatggagct gtatcatc 38

<210> 28

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> IgG1-B2M antisense construct

<400> 28

cggggtacct gaccaccgc ctcctttacc cggagacagg gagag 45

<210> 29

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> artificial sense primer to construct beta2-microglobulin

<400> 29

cggggtaccg gaggcggtgg gtcaatccag cgtactcca 39

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> artificial antisense primer to construct beta2-microglobulin

<400> 30

cgaccggtca tgtctcgatc ccactt 26

<210> 31

<211> 736

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric F(ab)-beta2-microglobulin

-15-

<400> 31
 gcggccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60
 cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc 120
 accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta 180
 cttccccgaa cgggtgacgg tgctgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240
 cttcccggtt gtcctacagt cctcaggact ctactccctc agcagcgctc tgaccgtgcc 300
 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360
 caaggtggac aagaaaggag gcggtgggtc aggtaccgga ggcggtgggt caatccagcg 420
 tactccaaag attcaggttt actcacgtca tccagcagag aatggaaagt caaatctcct 480
 gaattgctat gtgtctgggt ttcattccatc cgacattgaa gttgacttac tgaagaatgg 540
 agagagaatt gaaaaagtgg agcattcaga cttgtctttc agcaaggact ggtctttcta 600
 tctcttgtag tacactgaat tcacccccac tgaaaaagat gagtatgcct gccgtgtgaa 660
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 tcaccatcac cattga 736

<210> 32
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polypeptide sequence of the chimeric F(ab)-beta2-microglobulin
 <400> 32

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 85 90 95

-16-

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Gly Gly Gly Gly Ser Gly Thr
 115 120 125

Gly Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser
 130 135 140

Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val
 145 150 155 160

Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly
 165 170 175

Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Val Phe Ser Lys Asp
 180 185 190

Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys
 195 200 205

Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys
 210 215 220

Ile Val Lys Trp Asp Arg Asp Met Thr Gly His His His His His His
 225 230 235 240

<210> 33
 <211> 783
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the chimeric F(ab')₂-beta2-microglobulin

<400> 33
 gcggccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60
 cgcgcatatg gtcaccgtct cctcagcctc caaeaagggc ccatcgggtct tccccctggc 120
 accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta 180
 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240
 cttcccggtc gtcctacagt cctcaggact ctactccctc agcagcgctg tgaccgtgcc 300
 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360
 caaggtggac aagaaagttg agcccaaate ttgtgacaaa actcacacat gccaccgtg 420
 cccaggaggc ggtgggtcag gtaccggagg cgggtgggtca atccagcgta ctccaaagat 480
 tcaggtttac tcacgtcatc cagcagagaa tggaaagtca aatttcctga attgctatgt 540

-17-

```

gtctggggttt catccatccg acattgaagt tgacttactg aagaatggag agagaattga      600
aaaagtggag cattcagact tgtctttcag caaggactgg tctttctatc tcttgacta      660
cactgaattc acccccactg aaaagatgag tatgcctgcc gtgtgaacca tgtgactttg      720
tcacagccca agatagttaa gtgggatcga gacatgaccg gtcacatca ccatcaccat      780
tga                                                                    783

```

```

<210> 34
<211> 256
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Nucleotide sequence of the chimeric F(ab')2-beta2-microglobulin

```

```

<400> 34

```

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          20           25           30

```

```

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
          35           40           45

```

```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
          50           55           60

```

```

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
          65           70           75           80

```

```

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
          85           90           95

```

```

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
          100           105           110

```

```

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
          115           120           125

```

```

Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Gly Thr
          130           135           140

```

```

Gly Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser
          145           150           155           160

```

```

Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val

```

-18-

	165		170		175
Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly					
	180		185		190
Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Val Phe Ser Lys Asp					
	195		200		205
Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys					
	210		215		220
Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys					
	225		230		235
Ile Val Lys Trp Asp Arg Asp Met Thr Gly His His His His His His					
	245		250		255

<210> 35

<211> 1435

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric full IgG1-beta2 microglobulin

<400> 35

```

gcggcgcaaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg      60
cgcgcatatg gtcaccgtct ctcagcctc caccaagggc ccatcggtct tccccctggc      120
accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta      180
cttccccgaa ccggtgacgg tgctcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac      240
cttccccggt gtcctacagt ctcaggact ctactccctc agcagcgctc tgaccgtgcc      300
ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac      360
caaggtggac aagaaagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg      420
cccagcacct gaactcctgg ggggaccgtc agtcttcttc tccccccaa aaccaagga      480
caccctcatg atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga      540
agaccctgag gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac      600
aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct      660
gcaccaggac tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc      720
agccccatc gagaaaacca tctccaaagc caaagggcag ccccgagaac cacaggtgta      780
caccctgccc ccatcccgga atgagctgac caagaaccag gtcagcctga cctgcctggt      840
caaaggcttc tatccagcgc acatcgccgt ggagtgggag agcaatgggc agccggagaa      900

```

-19-

```

caactacaag accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa      960
gctcaccgtg gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca      1020
tgaggctctg cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaaggagg      1080
cgggtgggtca ggtaccggag .gcgggtgggtc aatccagcgt actccaaaga ttcaggttta      1140
ctcacgtcat ccagcagaga atggaaagtc aaatttcctg aattgctatg tgtctggggt      1200
tcatccatcc gacattgaag ttgacttact gaagaatgga gagagaattg aaaaagtgga      1260
gcattcagac ttgtctttca gcaaggactg gtctttctat ctcttgctact aactgaatt      1320
caccacctact gaaaaagatg agtatgcctg ccgtgtgaac catgtgactt tgtcacagcc      1380
caagatagtt aagtgggatc gagacatgac cggtcatcat caccatcacc attga          1435

```

<210> 36

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric full IgG1-beta2 microglobulin

<400> 36

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          20           25           30

```

```

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
          35           40           45

```

```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
          50           55           60

```

```

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
65           70           75           80

```

```

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
          85           90           95

```

```

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
          100          105          110

```

```

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
          115          120          125

```

```

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly

```

-20-

130		135		140
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile				
145		150	155	160
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu				
	165		170	175
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His				
	180		185	190
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg				
	195		200	205
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys				
	210		215	220
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu				
225		230	235	240
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr				
	245		250	255
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu				
	260		265	270
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp				
	275		280	285
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val				
	290		295	300
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp				
305		310	315	320
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His				
	325		330	335
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro				
	340		345	350
Gly Lys Gly Gly Gly Gly Ser Gly Thr Gly Gly Gly Gly Ser Ile Gln				
	355		360	365
Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly				
	370		375	380

-21-

Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp
 385 390 395 400

Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu
 405 410 415

His Ser Asp Leu Val Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr
 420 425 430

Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val
 435 440 445

Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp
 450 455 460

Met Thr Gly His His His His His His
 465 470

<210> 37
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer E1 Sense

<400> 37
 cacggtaccg atatggggtg cctgctgttt ctgc

34

<210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer E1 antisense

<400> 38
 cagaccggtc cagtagagga cgatgtcctg

30

<210> 39
 <211> 921
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Construct of extracellular domain of CD1d

<400> 39
 ggtaccgata tggggtgcct gctgtttctg ctgctctggg cgctcctcca ggcttgggga 60
 agcgctgaag tcccgc aaag gcttttcccc ctccgctgcc tccagatctc gtccttcgcc 120
 aatagcagct ggacgcgcac cgacggcttg gcgtggctgg gggagctgca gacgcacagc 180

-22-

```

tggagcaacg actcggacac cgtccgctct ctgaagcctt ggtcccaggg cacgttcagc   240
gaccagcagt gggagacgct gcagcatata tttcgggttt atcgaagcag cttcaccagg   300
gacgtgaagg aattcgccaa aatgctacgc ttatcctatc ccttggagct ccaggtgtcc   360
gctggctgtg aggtgcaccc tgggaacgcc tcaaataact tcttccatgt agcatttcaa   420
ggaaaagata tcctgagttt ccaaggaact tcttggggagc caaccaaga ggccccactt   480
tggtgtaaact tggccattca agtgctcaac caggacaagt ggacgagggg aacagtgcag   540
tggtcctta atggcacctg cccccaattt gtcagtggcc tccttgagtc aggggaagtcg   600
gaactgaaga agcaagtga gccaaggcc tggtgtgtcc gtggccccag tcctggccct   660
ggcgtctgc tgctggtgtg ccatgtctca ggattctacc caaagcctgt atgggtgaag   720
tggtatgcggg gtgagcagga gcagcagggc actcagccag gggacatcct gcccaatgct   780
gacgagacat ggtatctccg agcaaccctg gatgtggtgg ctggggaggg agctggcctg   840
tcctgtcggg tgaagcacag cagtctagag ggccaggaca tcgtcctcta ctggaccggt   900
catcatcacc atcaccattg a                                     921

```

<210> 40
 <211> 303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Construct of extracellular domain of CD1d

<400> 40

```

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
1               5               10              15

```

```

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
                20              25              30

```

```

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
    35              40              45

```

```

Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr
    50              55              60

```

```

Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
    65              70              75              80

```

```

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
    85              90              95

```

```

Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu

```

-23-

100 105 110
 Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser
 115 120 125
 Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
 130 135 140
 Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
 145 150 155 160
 Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val
 165 170 175
 Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
 180 185 190
 Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
 195 200 205
 Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
 210 215 220
 His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg
 225 230 235 240
 Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
 245 250 255
 Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
 260 265 270
 Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
 275 280 285
 Gln Asp Ile Val Leu Tyr Trp Thr Gly His His His His His His
 290 295 300

<210> 41

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> F(ab)-CD1d sense fragment

<400> 41

aattgcggcc gcaaaccatg ggatggagct gtatcatc

38

-24-

<210> 42
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> F(ab)-CD1d antisense fragment

<400> 42
cggggtacct gaccaccgc ctcctttcct gtccacctg gtgtt 45

<210> 43
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> F(ab')₂-CD1d sense fragment

<400> 43
aattgcggcc gcaaaccatg ggatggagct gtatcatc 38

<210> 44
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> F(ab')₂-CD1d antisense fragment

<400> 44
cggggtacct gaccaccgc ctcctgggca cgggtggcat gtgtg 45

<210> 45
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1-CD1d sense fragment

<400> 45
aattgcggcc gcaaaccatg ggatggagct gtatcatc 38

<210> 46
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1-CD1d antisense fragment

<400> 46
cggggtacct gaccaccgc ctcctttacc cggagacagg gagag 45

<210> 47
<211> 42

-25-

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sense primer to construct extracellular CD1d

<400> 47

cggggtaccg gaggcggtgg gtcagtcccg caaaggcttt tc 42

<210> 48

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial antisense primer to construct extracellular CD1d

<400> 48

cgaccggtcc agtagaggac gatgtcctg 29

<210> 49

<211> 1264

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric F(ab)-CD1d product

<400> 49

gcgccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60
 cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc 120
 accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta 180
 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240
 cttccccggt gtcctacagt cctcaggact ctactccctc agcagcgctc tgaccgtgcc 300
 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360
 caaggtggac aagaaaggag gcggtgggtc aggtaccgga ggcggtgggt cagtcccga 420
 aaggcttttc cccctccgct gcctccagat ctcgtccttc gccaatagca gctggacgcg 480
 caccgacggc ttggcgtggc tgggggagct gcagaegcac-agctggagca acgactcgga 540
 caccgtccgc tctctgaagc cttggtccca gggcacgttc agcgaccagc agtgggagac 600
 gctgcagcat atatttcggg tttatcgaag cagcttcacc agggacgtga aggaattcgc 660
 caaaatgcta cgcttatect atcccttgga gctccaggtg tccgctggct gtgaggtgca 720
 ccctgggaac gcctcaaata acttcttcca tgtagcattt caaggaaaag atatcctgag 780
 tttccaagga acttcttggg agccaaccca agaggcccca ctttgggtaa acttggccat 840
 tcaagtgtc aaccaggaca agtggacgag ggaaacagtg cagtggctcc ttaatggcac 900
 ctgcccccaa tttgtcagtg gcctccttga gtcagggaag tcggaactga agaagcaagt 960

-26-

```

gaagcccaag gcctggctgt cccgtggccc cagtctggc cctggccgtc tgctgctggt 1020
gtgccatgtc tcaggattct acccaaagcc tgtatgggtg aagtggatgc ggggtgagca 1080
ggagcagcag ggcactcagc caggggacat cctgccaat gctgacgaga catggtatct 1140
ccgagcaacc ctggatgtgg tggctgggga ggcagctggc ctgtcctgtc ggggaagca 1200
cagcagtcta gagggccagg acatcgctct ctactggacc ggatcatc accatcacca 1260
ttga 1264

```

```

<210> 50
<211> 416
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Polypeptide sequence of the chimeric F(ab)-CD1d product

```

```

<400> 50

```

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10           15

```

```

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
          20           25           30

```

```

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
          35           40           45

```

```

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
          50           55           60

```

```

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
        65           70           75           80

```

```

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
          85           90           95

```

```

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
          100           105           110

```

```

Pro Ser Asn Thr Lys Val Asp Lys Lys Gly Gly Gly Gly Ser Gly Thr
          115           120           125

```

```

Gly Gly Gly Gly Ser Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu
          130           135           140

```

```

Gln Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu
          145           150           155           160

```

-27-

Ala Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp
 165 170 175

Thr Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln
 180 185 190

Gln Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe
 195 200 205

Thr Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro
 210 215 220

Leu Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala
 225 230 235 240

Ser Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser
 245 250 255

Phe Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val
 260 265 270

Asn Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr
 275 280 285

Val Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu
 290 295 300

Leu Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala
 305 310 315 320

Trp Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val
 325 330 335

Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met
 340 345 350

Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro
 355 360 365

Asn Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala
 370 375 380

Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu
 385 390 395 400

Gly Gln Asp Ile Val Leu Tyr Trp Thr Gly His His His His His His
 405 410 415

-28-

<210> 51
 <211> 1312
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of the chimeric F(ab')₂-CD1d product

<400> 51
 gcggccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60
 cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc 120
 accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta 180
 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240
 cttccccggct gtcttacagt cctcaggact ctactccctc agcagcgctc tgaccgtgcc 300
 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360
 caaggtggac aagaaagttg agcccaaate ttgtgacaaa actcacacat gcccaccgtg 420
 cccaggaggc ggtgggtcag gtaccggagg cgggtgggtca gtcccgcaaa ggcttttccc 480
 cctccgctgc ctccagatct cgtccttcgc caatagcagc tggacgcgca ccgacggctt 540
 ggctggtcgtg ggggagctgc agacgcacag ctggagcaac gactcggaca ccgtccgctc 600
 tctgaagcct tgggtcccagg gcacgttcag cgaccagcag tgggagacgc tgcagcatat 660
 atttcgggtt tatcgaagca gcttcaccag ggacgtgaag gaattcgcca aaatgctacg 720
 cttatcctat cccttggagc tccaggtgtc cgctggctgt gaggtgcacc ctgggaacgc 780
 ctcaaataac ttcttccatg tagcatttca aggaaaagat atcctgagtt tccaaggaac 840
 ttcttgggag ccaacccaag agggccctact ttgggtaaac ttggccattc aagtgtctaa 900
 ccaggacaag tggacgaggg aaacagtgcg gtggctcctt aatggcacct gcccccaatt 960
 tgtcagtggc ctcccttgagt caggggaagtc ggaactgaag aagcaagtga agcccaagggc 1020
 ctggctgtcc cgtggcccca gtcttgccc tggccgtctg ctgctggtgt gccatgtctc 1080
 aggattctac ccaaagcctg tatgggtgaa gtggatgcgg ggtgagcagg agcagcaggg 1140
 cactcagcca ggggacatcc tgcccaatgc tgacgagaca tggatatctc gagcaaccct 1200
 ggatgtggtg gctggggagg cagctggcct gtcctgtcgg gtgaagcaca gcagtctaga 1260
 gggccaggac atcgtcctct actggaccgg tcatcatcac catcaccatt ga 1312

<210> 52
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polypeptide sequence of the chimeric F(ab')₂-CD1d product

-29-

<400> 52

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Gly Ser Gly Thr
 130 135 140

Gly Gly Gly Gly Ser Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu
 145 150 155 160

Gln Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu
 165 170 175

Ala Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp
 180 185 190

Thr Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln
 195 200 205

Gln Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe
 210 215 220

Thr Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro
 225 230 235 240

Leu Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala .
245 250 255

Phe Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val
275 280 285

Val Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu
305 310 315 320

Leu Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala
325 330 335

Trp Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val
340 345 350

Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met
355 360 365

Arg Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro
370 375 380

Asn Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala
385 390 395 400

Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu
405 410 415

Gly Gln Asp Ile Val Leu Tyr Trp Thr Gly His His His His His His
420 425 430

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<210> 53
<211> 1963
<212> DNA
<213> Artificial Sequence
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<220>
<223> Nucleotide sequence of the chimeric IgG1-CD1d product

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<400> 53
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cgcgcatatg gtcaccgtct cctcagcctc caccaagggc ccatcggtct tccccctggc      120
accctcctcc aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta      180

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-31-

cttccccgaa	ccggtgacgg	tgtcgtggaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac	240
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ctccagcagc	ttgggcaccc	agacctacat	ctgcaacgtg	aatcacaagc	ccagcaacac	360
caagggtggac	aagaaagttg	agcccaaatac	ttgtgacaaa	actcacacat	gcccaccgtg	420
cccagcacct	gaactcctgg	ggggaccgtc	agtcttcctc	ttccccccaa	aacccaagga	480
caccctcatg	atctcccggg	cccctgaggt	cacatgcgtg	gtggtggacg	tgagccacga	540
agaccctgag	gtcaagttca	actggtacgt	ggacggcggtg	gaggtgcata	atgccaagac	600
aaagccgcgg	gaggagcagt	acaacagcac	gtaccgtgtg	gtcagcgtec	tcaccgtcct	660
gcaccaggac	tggctgaatg	gcaaggagta	caagtgcaag	gtctccaaca	aagccctccc	720
agccccatc	gagaaaacca	tctccaaagc	caaagggcag	ccccgagaac	cacaggtgta	780
caccctgccc	ccatcccggg	atgagctgac	caagaaccag	gtcagcctga	cctgcctggt	840
caaaggcttc	tatcccagcg	acatcgccgt	ggagtgggag	agcaatgggc	agccggagaa	900
caactacaag	accacgcctc	ccgtgctgga	ctccgacggc	tccttcttcc	tctacagcaa	960
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cgggtgggtca	ggtaccggag	gcggtgggtc	agtcccgcaa	aggcttttcc	ccctccgctg	1140
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ggctggggag	gcagctggcc	tgtcctgtcg	ggtgaagcac	agcagtctag	agggccagga	1920
catcgctctc	tactggaccg	gtcatcatca	ccatcaccat	tga		1963

-32-

<211> 649

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide sequence of the IgG1CD1d product

<400> 54

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
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Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys

-33-

210	215	220
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu 225 230 235 240		
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr 245 250 255		
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu 260 265 270		
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp 275 280 285		
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val 290 295 300		
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp 305 310 315 320		
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His 325 330 335		
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 340 345 350		
Gly Lys Gly Gly Gly Gly Ser Gly Thr Gly Gly Gly Gly Ser Val Pro 355 360 365		
Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln Ile Ser Ser Phe Ala Asn 370 375 380		
Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala Trp Leu Gly Glu Leu Gln 385 390 395 400		
Thr His Ser Trp Ser Asn Asp Ser Asp Thr Val Arg Ser Leu Lys Pro 405 410 415		
Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln Trp Glu Thr Leu Gln His 420 425 430		
Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr Arg Asp Val Lys Glu Phe 435 440 445		
Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu Glu Leu Gln Val Ser Ala 450 455 460		

-34-

Gly Cys Glu Val His Pro Gly Asn Ala Ser Asn Asn Phe Phe His Val
 465 470 475 480

Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe Gln Gly Thr Ser Trp Glu
 485 490 495

Pro Thr Gln Glu Ala Pro Leu Trp Val Asn Leu Ala Ile Gln Val Leu
 500 505 510

Asn Gln Asp Lys Trp Thr Arg Glu Thr Val Gln Trp Leu Leu Asn Gly
 515 520 525

Thr Cys Pro Gln Phe Val Ser Gly Leu Leu Glu Ser Gly Lys Ser Glu
 530 535 540

Leu Lys Lys Gln Val Lys Pro Lys Ala Trp Leu Ser Arg Gly Pro Ser
 545 550 555 560

Pro Gly Pro Gly Arg Leu Leu Leu Val Cys His Val Ser Gly Phe Tyr
 565 570 575

Pro Lys Pro Val Trp Val Lys Trp Met Arg Gly Glu Gln Glu Gln Gln
 580 585 590

Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn Ala Asp Glu Thr Trp Tyr
 595 600 605

Leu Arg Ala Thr Leu Asp Val Val Ala Gly Glu Ala Ala Gly Leu Ser
 610 615 620

Cys Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Val Leu Tyr
 625 630 635 640

Trp Thr Gly His His His His His His
 645